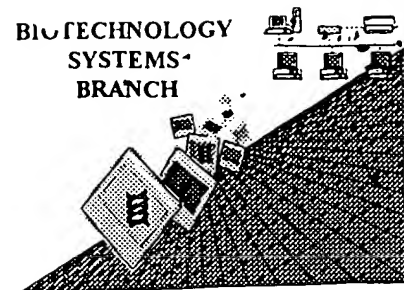


BEST AVAILABLE COPY

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09934060

Source: OIPE

Date Processed by STIC: 09.07.2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ^{OK}ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09 934 060

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

40/

OIPE

RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/934,060

TIME: 16:20:40

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

3 <110> APPLICANT: DeVico et al, Anthony
 5 <120> TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
 7 <130> FILE REFERENCE: 4115-144 CIP
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/934,060
 C--> 9 <141> CURRENT FILING DATE: 2001-08-21.
 9 <160> NUMBER OF SEQ ID NOS: 33
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2159
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: Synthesized construct ✓
 21 <400> SEQUENCE: 1

| | | | | | | | |
|----|-------------|-------------|------------|------------|-------------|-------------|------|
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| 24 | tcctgcctcg | gaaacgccga | ggagaagctg | tgggtgaccg | tgtactacgg | cgtgcccgtg | 120 |
| 26 | tggaaggagg | ccaccaccac | cctgttctgc | gccagcgacc | gcaaggccta | cgacaccgag | 180 |
| 28 | gtgcacaacg | tgtggggccac | ccacgcctgc | gtgcccaccg | acccaaccc | ccaggagggtg | 240 |
| 30 | gagctgaaga | acgtgaccga | gaacttcaac | atgtggaaga | acaacatggt | ggagcagatg | 300 |
| 32 | cacgaggaca | tcacagcct | gtgggaccag | agcctgaagc | cctgcgtgaa | gctgaccccc | 360 |
| 34 | ctgtgcgtga | ccctgaactg | caccgacctg | cgcaacgcca | ccaacggcaa | cgacaccaac | 420 |
| 36 | accactagta | gcagccgcgg | catggtgggc | ggcggcgaga | tgaagaactg | cagcttcaac | 480 |
| 38 | atcaccacca | acatccgcgg | caaggtgcag | aaggagtacg | ccctgttcta | caagctggac | 540 |
| 40 | atcgccccca | tcgacaacaa | cagcaacaac | cgctaccgcc | tgatcagctg | caacaccagc | 600 |
| 42 | gtgatcaccc | aggcctgccc | caaggtgagc | ttcgagccca | tccccatcca | ctactgcgcc | 660 |
| 44 | cccgcgggct | tcgccatcct | gaagtgcag | gacaagaagt | tcaacggcaa | gggcccctgc | 720 |
| 46 | accaacgtga | gcaccgtgca | gtgcaccac | ggcatccgcc | ccgtggtgag | caccagctg | 780 |
| 48 | ctgctgaacg | gcagcctggc | cgaggaggag | gtggtgatcc | gcagcgccaa | cttcgcccag | 840 |
| 50 | aacgccaaag | tgatcatcgt | gcagctgaac | gagagcgtgg | agatcaactg | caccgccccc | 900 |
| 52 | aacaacaaca | cccgcaagtc | catccacatc | ggccccggcc | gcgccttcta | caccaccggc | 960 |
| 54 | gagatcatcg | gcgacatccg | ccaggcccac | tgcaacctga | gccgcgccaa | gtggaacgac | 1020 |
| 56 | accctgaaca | agatcgtgat | caagctgcgc | gagcagttcg | gcaacaagac | catcgtgttc | 1080 |
| 58 | aagcacagca | gcggcgggcg | ccccgagatc | gtgaccacaa | gcttcaattg | cggcggcgag | 1140 |
| 60 | ttctttctact | gcaacagcac | ccagctgttc | aacagcacct | ggaacgtgac | cgaggagagc | 1200 |
| 62 | aacaacaccg | tggagaacaa | caccatcacc | ctgccctgcc | gcatcaagca | gatcatcaac | 1260 |
| 64 | atgtggcagg | aggtggggccg | cgccatgtac | gcccccccca | tcgcgcggcca | gatccgctgc | 1320 |
| 66 | agttchaaca | tcaccggcct | gctgctgacc | cgcgacggcg | gccccgagga | caacaagacc | 1380 |
| 68 | gaggtgttcc | gccccggcgg | cggcgacatg | cgcgacaact | ggcgcagcga | gctgtacaag | 1440 |
| 70 | tacaagggtg | tgaagatcga | gccccctggc | gtggccccca | ccaaggccaa | gcgcgcgctg | 1500 |
| 72 | gtgcagcgcg | agaagcgtgg | atcctctggt | ggcgggtggc | cgggctccgg | aggaggtggg | 1560 |
| 74 | tcgggtggcg | gcgcggccgc | taagaaagtg | gtgctgggca | aaaaagggga | tacagtggaa | 1620 |
| 76 | ctgacctgta | cagcttccca | gaagaagagc | atacaattcc | actggaaaaa | ctccaaccag | 1680 |
| 78 | ataaagattc | tgggaaatca | gggtcccttc | ttaactaaag | gtccatccaa | gctgaatgat | 1740 |
| 80 | cgcgctgact | caagaagaag | cctttgggac | caaggaaact | tccccctgat | catcaagaat | 1800 |
| 82 | cttaagatag | aagactcaga | tacttacatc | tgtgaagtgg | aggaccagaa | ggaggagggtg | 1860 |
| 84 | caattgctag | tgttcggatt | gactgccaac | tctgacaccc | acctgcttca | ggggcagagc | 1920 |
| 86 | ctgaccctga | ccttgagag | ccccctggt | agtagccct | cagtgcgaatg | taggagtcca | 1980 |

Does Not Comply
 Corrected Diskette Needed
See page 2 of 7

RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/934,060

TIME: 16:20:40

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

88 aggggtaaaa acatacaggg ggggaagacc ctctccgtgt ctacagctgga gctccaggat 2040
 90 agtggcacct ggacatgcac tgtcttgacg aaccagaaga aggtggagtt caaaatagac 2100
 92 atcgtggtgc tagctgaaca aaaactcatc tcagaagagg atctgtaata tgtttaaac 2159

95 <210> SEQ ID NO: 2

96 <211> LENGTH: 720

97 <212> TYPE: PRT

98 <213> ORGANISM: Artificial Sequence

100 <220> FEATURE:

101 <223> OTHER INFORMATION: Synthesized construct

103 <220> FEATURE:

104 <221> NAME/KEY: MISC_FEATURE

105 <223> OTHER INFORMATION: X can

108 <220> FEATURE:

109 <221> NAME/KEY: MISC_FEATURE

110 <222> LOCATION: (716)..(716)

111 <223> OTHER INFORMATION: X can

114 <220> FEATURE:

115 <221> NAME/KEY: MISC_FEATURE

116 <222> LOCATION: (719)..(719)

117 <223> OTHER INFORMATION: X can be any amino acid

120 <400> SEQUENCE: 2

122 Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
 123 1 5 10 15
 126 Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
 127 20 25 30
 130 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
 131 35 40 45
 134 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
 135 50 55 60
 138 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
 139 65 70 75 80
 142 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
 143 85 90 95
 146 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
 147 100 105 110
 150 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
 151 115 120 125
 154 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
 155 130 135 140
 158 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
 159 145 150 155 160
 162 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
 163 165 170 175
 166 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
 167 180 185 190
 170 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
 171 195 200 205
 174 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
 175 210 215 220

Invalid 223 response
 if unknown
 must be enumerated
 in fields 221, 223
 and 223. Specifically
 to express location
 and placement in
 the gene sequence.

Errored

Errored

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/934,060

DATE: 09/07/2001

TIME: 16:20:40

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

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178 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
179 225                230                235                240
182 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
183                245                250                255
186 Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
187                260                265                270
190 Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
191                275                280                285
194 Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
195                290                295                300
198 Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
199 305                310                315                320
202 Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
203                325                330                335
206 Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
207                340                345                350
210 Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Asp Pro
211                355                360                365
214 Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
215                370                375                380
218 Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
219 385                390                395                400
222 Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
223                405                410                415
226 Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
227                420                425                430
230 Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
231                435                440                445
234 Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
235                450                455                460
238 Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
239 465                470                475                480
242 Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
243                485                490                495
246 Lys Arg Arg Val Val Gln Arg Glu Lys Arg Gly Ser Ser Gly Gly Gly
247                500                505                510
250 Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Lys
251                515                520                525
254 Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
255                530                535                540
258 Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
259 545                550                555                560
262 Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
263                565                570                575
266 Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
267                580                585                590
270 Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
271                595                600                605
274 Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/934,060

DATE: 09/07/2001

TIME: 16:20:40

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

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275      610      615      620
278 Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
279 625      630      635      640
282 Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
283      645      650      655
286 Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
287      660      665      670
290 Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
291      675      680      685
294 Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
295      690      695      700
W--> 298 Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
299 705      710      715      720
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 2159
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Synthesized construct
310 <400> SEQUENCE: 3
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313 tcctgcctcg gaaacgcgca ggagaagctg tgggtgaccg tgtactacgg cgtgcccgtg      120
315 tggaaaggag ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag      180
317 gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg      240
319 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggg ggagcagatg      300
321 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc      360
323 ctgtgcgtga ccctgaactg caccgacctg cgcaacgcca ccaacggcaa cgacaccaac      420
325 accactagta gcagccgcgg catgggtggc ggcgcgaga tgaagaactg cagcttcaac      480
327 atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac      540
329 atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc      600
331 gtgatcaccg aggcctgcc caaggtgagc ttcgagccca tccccatcca ctactgcgc      660
333 cccgccggct tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc      720
335 accaactgta gcaccgtgca gtgcaccac ggcatccgcc ccgtggtgag caccagctg      780
337 ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgcaa cttcgcgcgac      840
339 aacgccaaag tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc      900
341 aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc      960
343 gagatcatcg gcgacatccg ccaggccccac tgcaacctga gccgcgcaa gtggaacgac      1020
345 accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc      1080
347 aagcacagca gcggcggcga ccccgagatc gtgaccaca gttcaattg cggcggcgag      1140
349 ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc      1200
351 aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac      1260
353 atgtggcagg aggtgggccc cgccatgtac gcccccccca tccgcggcca gatccgtgc      1320
355 agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc      1380
357 gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag      1440
359 tacaaggtgg tgaagatcga gcccttgggc gtggccccc ccaaggccaa gcgcccgtg      1500
361 gtgcagcgcg agaagaccgg atcctctggt ggcggtggct cgggctccgg aggaggtgg      1560
363 tcgggtggcg gcgcggccgc taagaaagtg gtgctgggca aaaaagggga tacagtggaa      1620
365 ctgacctgta cagcttccca gaagaagagc atacaattcc actggaaaaa ctccaaccag      1680
367 ataaagattc tgggaaatca gggctccttc ttaactaaag gtccatccaa gctgaatgat      1740

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RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/934,060

TIME: 16:20:40

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

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369 cgcgctgact caagaagaag cctttgggac caaggaaact tccccctgat catcaagaat 1800
371 ctttaagatag aagactcaga tacttacatc tgtgaagtgg aggaccagaa ggaggagggtg 1860
373 caattgctag tggttcggatt gactgccaac tctgacaccc acctgcttca ggggcagagc 1920
375 ctgaccctga ccttggagag cccccctggt agtagccctt cagtgcattg taggagtcca 1980
377 aggggtaaaa acatacaggg ggggaagacc ctctccgtgt ctcagctgga gctccaggat 2040
379 agtggcacct ggacatgcac tgtcttgagc aaccagaaga aggtggagtt caaaatagac 2100
381 atcgtggtgc tagctgaaca aaaactcatc tcagaagagg atctgtaata tgtttaaac 2159
384 <210> SEQ ID NO: 4
385 <211> LENGTH: 720
386 <212> TYPE: PRT
387 <213> ORGANISM: Artificial Sequence
389 <220> FEATURE:
390 <223> OTHER INFORMATION: Synthesized construct
392 <220> FEATURE:
393 <221> NAME/KEY: MISC_FEATURE
394 <222> LOCATION: (716)..(720)
395 <223> OTHER INFORMATION: X can be any amino acid
398 <400> SEQUENCE: 4
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404 Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
405 20 25 30
408 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
409 35 40 45
412 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
413 50 55 60
416 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
417 65 70 75 80
420 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
421 85 90 95
424 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
425 100 105 110
428 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
429 115 120 125
432 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
433 130 135 140
436 Ser Arg Gly Met Val Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
437 145 150 155 160
440 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
441 165 170 175
444 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
445 180 185 190
448 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
449 195 200 205
452 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
453 210 215 220
456 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
457 225 230 235 240
460 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val

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VERIFICATION SUMMARY

DATE: 09/07/2001

PATENT APPLICATION: US/09/934,060

TIME: 16:20:41

Input Set : A:\cd4m9-DevicoST25.txt

Output Set: N:\CRF3\09072001\I934060.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:811 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:843 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:863 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:2016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32